

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 09:23:04 ; Search time 592 Seconds  
(without alignments)  
10369.125 Million cell updates/sec

Title: US-09-494-297-1  
2274  
Perfect score: 1 atgaaaaaaaggttcc.....ggatagaagaacatgactag 2274  
Sequence:

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

N\_Geneseq.19Jun03:\*

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2:	/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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25:	/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2271	99.9	2286	24	ABN69678
2	75	3.3	159	24	ABN69679
3	56.6	2.5	4677	21	AAA70259
4	56.6	2.5	32392	24	ABL56203
5	56.2	2.5	34688	24	ABO67060
6	56	2.5	11922	21	AAA70187
7	53.8	2.4	5940	21	AAA70105
8	53	2.3	494	23	ABV10021

9	53	2.3	335913	22	AA161371
10	53	2.3	335913	22	AA161372
11	52.8	2.3	8210	24	ABL70331
12	52.8	2.3	8210	24	AA61282
13	52.8	2.3	8210	24	ABK3180
14	52.4	2.3	6106	22	AA546429
15	52.4	2.3	6106	22	ABK40031
16	52.4	2.3	6106	24	ABL33472
17	52.2	2.3	50000	24	ABL56203
18	52	2.3	7195	22	AA545325
19	52	2.3	7195	22	ABK28166
20	52	2.3	37515	24	ABO66998
21	51.4	2.3	1998	21	AAA70212
22	51.2	2.3	1527	21	AAA70121
23	51.2	2.3	3399	17	AA05868
24	51.2	2.3	4985	24	ABO75107
25	51	2.2	8056	25	ABZ10100
26	50.6	2.2	4590	22	AAH24065
27	50.6	2.2	6815	22	AA545345
28	50.6	2.2	6815	24	ABL32671
29	50.6	2.2	6815	24	ABK28176
30	50.6	2.2	7819	24	ABL33953
31	50.6	2.2	7819	24	ABL34607
32	50.2	2.2	15016	20	AAK99560
33	50.2	2.2	19087	24	ABL32793
34	50	2.2	2000	24	ABZ14930
35	50	2.2	6381	24	ABL70243
36	50	2.2	6381	24	ABL2966
37	50	2.2	6381	24	ABL34518
38	50	2.2	640681	24	ABA92787
39	49.8	2.2	50000	24	ABL56203
40	49.8	2.2	50000	24	ABL56201
41	49.6	2.2	3095	11	AA03875
42	49.6	2.2	12705	24	ABL2148
43	49.4	2.2	15251	24	ABO76622
44	49.2	2.2	34548	24	ABL70603
45	49	2.2	16724	24	ABL70259

## ALIGNMENTS

RESULT 1  
ABN69678  
ID ABN69678 standard; DNA; 2286 BP.  
XX  
AC ABN69678;  
XX  
XX  
DT 01-JUN-2002 (first entry)  
XX  
DE Streptococcus polynucleotide SEQ ID NO 7269.  
XX  
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;  
KW antinflammatory; Infection; vaccine; meningitis; gene therapy; ds.  
XX  
XX Streptococcus pyogenes  
XX  
XX (MO20023471.1.A2)  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB04789.  
XX  
PR 27-OCT-2000; 2000GB-0026333.  
PR 24-NOV-2000; 2000GB-0028727.  
PR 07-MAR-2001; 2001GB-0005640.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
PI Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C;  
Tetrelin H;

Soybean 240017 reg  
Soybean 240017 reg.  
Chemically treated  
Human gene regulat  
Signal transductio  
Tumour suppressor  
Human chemically p  
Human immune syste  
AMEPV genome fragm  
Chemically pretrea  
DNA transcripion  
Human angiogenes  
Plasmodium falci  
Chicken leucocyt  
Anopheles gamb  
Haematopoietic cel  
Yeast AOD9604-asso  
Chemically pretrea  
Human immune syste  
DNA transcripion  
Human immune syste  
Human metastasis a  
Nucleic acid sequ  
Human immune syste  
Arabidopsis thalia  
Chemically treated  
Human immune syste  
Human metastasis a  
Buchnera sp. genom  
AMEPV genome fragm  
Sequence encoding  
Human immune syste  
C. albicans BAX-as  
Chemically treated  
Chemically treated

1087

QY	601	GAAAGTTTTAAAGGGAGTCAGAAAGTAACCTGGTTAGTACCTTCCATATATCTTTGATG	660
Db	616	GAAAGTTTTAAAGGGAGTCAGAAAGTAACCTGGTTAGTACCTTCCATATATCTTTGATG	675
QY	661	CGTCACCTTTGAAGCACTGATTTGATCCGAATTTGGCACTAAATATGCCAAACAAGTT	720
Db	676	CGTCACCTTTGAAGCACTGATTTGATCCGAATTTGGCACTAAATATGCCAAACAAGTT	735
QY	721	CCGGATATTTTTCAGCTAAGATATTTTTCAGCTAGGCAAGGGAGATTAATATATATATA	780
Db	736	CCGGATATTTTTCAGCTAAGATATTTTTCAGCTAGGCAAGGGAGATTAATATATATATA	795
QY	781	GGATACCAAAATCTTTTAGTGTGTGTATTTAGTTCTCTAAACCACCAACTCCAGAGAC	840
Db	796	GGATACCAAAATCTTTTAGTGTGTGTATTTAGTTCTCTAAACCACCAACTCCAGAGAC	855
QY	841	CCACCAATGCCCTCCAAATCAACCTCAAAACGACTTCAGTACTTATTAGAAATATGCTATA	900
Db	856	CCACCAATGCCCTCCAAATCAACCTCAAAACGACTTCAGTACTTATTAGAAATATGCTATA	915
QY	901	GGGATATACCTTAATTTGCTTGAAGGTCGAACATTAACGTTGACAGGGGATTAACGTGAT	960
Db	916	GGGATATACCTTAATTTGCTTGAAGGTCGAACATTAACGTTGACAGGGGATTAACGTGAT	975
QY	961	AGTTTTCACGACGAGTGTATTAGCAGTAATGATTTGGAGAAAGATTTGAACATACAGAT	1020
Db	976	AGTTTTCACGACGAGTGTATTAGCAGTAATGATTTGGAGAAAGATTTGAACATACAGAT	1035
QY	1021	GGAACTATATCTTAACTGAAATTTGAATTTCTCCACTGGTTATAGTATTCGACAGCCATTC	1080
Db	1036	GGAACTATATCTTAACTGAAATTTGAATTTCTCCACTGGTTATAGTATTCGACAGCCATTC	1095
QY	1081	ACCTTTAAGGTTGAAGTCGGCAAGTCGTATCTATTATTTGATGCAAAACAGATTGAAAT	1140
Db	1096	ACCTTTAAGGTTGAAGTCGGCAAGTCGTATCTATTATTTGATGCAAAACAGATTGAAAT	1155
QY	1141	CCCAATTAAGAGATAGTAGAGCCCTTACTCAGTAGAAGCATATATGATTTTGAAGAATTT	1200
Db	1156	CCCAATTAAGAGATAGTAGAGCCCTTACTCAGTAGAAGCATATATGATTTTGAAGAATTT	1215
QY	1201	AGCCTTTTAACTACACAAACTATATGCAATTTTATTTGCAAAAAATTAATAATGGAAGT	1260
Db	1216	AGCCTTTTAACTACACAAACTATATGCAATTTTATTTGCAAAAAATTAATAATGGAAGT	1275
QY	1261	TCACAGGTCGCTATTTGCTTTAATGACAGATCTAAATATCCACGCGATCTGGAAGATGCT	1320
Db	1276	TCACAGGTCGCTATTTGCTTTAATGACAGATCTAAATATCCACGCGATCTGGAAGATGCT	1335
QY	1321	GGGAAAAACAATGATCCAGACTTTTACAAACAGAGAGATTAATACTCATATTTGCAGGT	1380
Db	1336	GGGAAAAACAATGATCCAGACTTTTACAAACAGAGAGATTAATACTCATATTTGCAGGT	1395
QY	1381	CGTAGACCTCTTTAAATATATCTGTGAAACCAAGAGATCCGATCCTGACACATTTCTTAAA	1440
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QY	1441	CATATCAAAAAAGTAATTTGAGAAGGTCACAGGGAAAAAGGAAACAAGCATTTAGATATGT	1500
Db	1456	CATATCAAAAAAGTAATTTGAGAAGGTCACAGGGAAAAAGGAAACAAGCATTTAGATATGT	1515
QY	1501	GGTCTAATCGAGACAAATTGCGTGGCGCTACTCAGTTAGCAATATATATTATTTCACTGAT	1560
Db	1516	GGTCTAATCGAGACAAATTGCGTGGCGCTACTCAGTTAGCAATATATATTATTTCACTGAT	1575
QY	1561	AGTCTGAATTTAGATTAAGGATTAACCTAAAGACATATCATGCTTTTGGACATGATGAT	1620
Db	1576	AGTCTGAATTTAGATTAAGGATTAACCTAAAGACATATCATGCTTTTGGACATGATGAT	1635
QY	1621	AGTACTTATAGCAGTTGCTAAATATCCTCTGTAGATAATACGTCGAAGATAGTAATCTCCACAG	1680
Db	1636	AGTACTTATAGCAGTTGCTAAATATCCTCTGTAGATAATACGTCGAAGATAGTAATCTCCACAG	1695

OY	1661	CTAATGACCCGTGATTTCTTTATTCGCCGATTAACATATAATATTCATCTCTTATGGAACT	1740
Db	1696	CTAACTGACCTGTGATTTCTTTATTCGCCGATTAACATATAATATTCATCTCTTATGGAACT	1755
OY	1741	CAGTGGCATCCAGAAGATTTAGTTGATTTATTCGTATGGAAGATTAATAAAGAAAGTTATA	1800
Db	1756	CAGTGGCATCCAGAAGATTTAGTTGATTTATTCGTATGGAAGATTAATAAAGAAAGTTATA	1815
OY	1801	CCTGTAACTCTAATTTTAACTTTAGAGAAAAACGGTGACTGGTTTACGCTGTGACAGAACT	1860
Db	1816	CCTGTAACTCTAATTTTAACTTTAGAGAAAAACGGTGACTGGTTTACGCTGTGACAGAACT	1875
OY	1861	AAAGATTTCCATTTTGGAAATTTGATTTAAAAATTAATTAAGCAAGATTGCTTTCGAACT	1920
Db	1876	AAAGATTTCCATTTTGGAAATTTGATTTAAAAATTAATTAAGCAAGATTGCTTTCGAACT	1935
OY	1921	GTTTAAAAACAGTAAACAAACCTCGAATTTTAAAGATGTAAAGCAACATTAATTTAAA	1980
Db	1936	GTTTAAAAACAGTAAACAAACCTCGAATTTTAAAGATGTAAAGCAACATTAATTTAAA	1995
OY	1981	CATGGGGAAAGTTTAAACCTTCAAGGTTTACAGAAAGTTTATTTCTTACCTTGTCAAAGAA	2040
Db	1996	CATGGGGAAAGTTTAAACCTTCAAGGTTTACAGAAAGTTTATTTCTTACCTTGTCAAAGAA	2055
OY	2041	ACAGATTTGGAAGGCTTAAAGCTTAAAGTTAAATGCCAAGAAAGTACGATCGTACAGTT	2100
Db	2056	ACAGATTTGGAAGGCTTAAAGGCTTAAAGTTAAATGCCAAGAAAGTACGATCGTACAGTT	2115
OY	2101	TCAAAACACAGAAATACACAGTATGAGACACTTACTTTTGAAATTAATTAAGAACCCGTT	2160
Db	2116	TCAAAACACAGAAATACACAGTATGAGACACTTACTTTTGAAATTAATTAAGAACCCGTT	2175
OY	2161	GTTCCCTACAGAGTTGATCAAAAGATCAATGGCTATCTAGCTTTGATAGTTATGCGTGT	2220
Db	2176	GTTCCCTACAGAGTTGATCAAAAGATCAATGGCTATCTAGCTTTGATAGTTATGCGTGT	2235
OY	2221	ATCAGTTTGGGAGATCTGGGGAATTCACACGTAAGTAAGTAAGAAACATGAC	2271
Db	2236	ATCAGTTTGGGAGATCTGGGGAATTCACACGTAAGTAAGTAAGAAACATGAC	2286

XX	ABN69679/c
XX	ID ABN69679 standard; DNA; 159 BP.
XX	AC
XX	ABN69679;
XX	DJ
XX	01-JUL-2002 (first entry)
DE	Streptococcus polynucleotide SEQ ID NO 7271.
XX	KW Streptococcus GAS; GBS; group B streptococcus; Streptococcus agalactiae
KW	group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KM	antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX	OS Streptococcus pyogenes.
XX	PV WO200234771-A2.
XX	PD
XX	02-MAY-2002.
PP	29-OCT-2001; 2001WO-GB04789.
XX	PR 27-OCT-2000; 2000GB-0026333.
PR	24-NOV-2000; 2000GB-0028727.
PR	07-MAR-2001; 2001GB-0005640.
XX	PA
PA	(CHIR-) CHIRON SPA.
XX	(GENO-) INST GENOMIC RES.
PI	Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C,
PI	Tetelin H;
XX	

DR MPI: 2002-352536/38.  
 DR P-PSDB: ABP29048.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX  
 PS Claim 7; Page 38/79; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and anti-inflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.  
 XX  
 SO Sequence 159 BP; 46 A; 31 C; 27 G; 55 T; 0 other;

	Query Match	3.3%	Score 75;	DB 24;	Length 159;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-07;		
	Matches	75; Conservative	0; Mismatches	0; Indels	0; Gaps
OY	2200	GCTTGGATAGATTATTCGCTGTATCATCGTTGGGCACTCTGGGAATCACACGTAAGGATA	225		
Db	159	GCTTGGATAGATTATTCGCTGTATCATCGTTGGGCACTCTGGGAATCACACGTAAGGATA	100		
OY	2260	AGAAACATGACTAG 2274			
Db	99	AGAAACATGACTAG 85			

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XX RESULT 3
XX ID AAA70259 standard; pNA: 4677 BP.
XX AAA70259;
XX
XX 07-NOV-2000 (first entry)
XX
XX Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:392
XX
XX Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
XX antimalarial; malaria; protozoacide; infection; insecticide; ds.
XX
XX Plasmodium falciparum.
XX
XX WO200025728-A2.
XX
XX
XX 11-MAY-2000.
XX
XX 05-NOV-1999; 99WO-US26796.
XX
XX 05-NOV-1998; 98US-0107131.
XX
XX (HOEF/) HOFFMAN S.
XX (CARU/) CARUCCI D.
XX (GARD/) GARDNER M.
XX (VENT/) VENTER J C.
XX
XX Hoffman S, Carucci D, Gardner M, Venter JC;
XX WPI: 2000-365347/31.
XX

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